

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/559,627  
Source: IFWP  
Date Processed by STIC: 12/16/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/559,627

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering            The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII            The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please ensure your subsequent submission is saved in **ASCII text**.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"                A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)        Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)        Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)        Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10     Invalid <213>  
    Response            Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11     Use of <220>        Sequence(s)              missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12     PatentIn 2.0  
    "bug"                Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13     Misuse of n/Xaa    "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,627

TIME: 15:34:28

Input Set : A:\seq list.txt

Output Set : N:\CRF4\12162005\J559627.raw

3 <110> APPLICANT: ARDUINI, Arduino  
 4 PATRIZI, Andrea  
 6 <120> TITLE OF INVENTION: Therapeutic and diagnostic means for papillomas and other diseases  
 7 involving PED/PEA-15  
 9 <130> FILE REFERENCE: 2818-248  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/559,627  
 12 <141> CURRENT FILING DATE: 2005-12-06  
 15 <150> PRIOR APPLICATION NUMBER: PCT/IT2004/000325  
 16 <151> PRIOR FILING DATE: 2004-06-03  
 19 <150> PRIOR APPLICATION NUMBER: RM 2003 A 000283  
 20 <151> PRIOR FILING DATE: 2003-06-06  
 22 <160> NUMBER OF SEQ ID NOS: 4  
 24 <170> SOFTWARE: PatentIn version 3.1  
 26 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 20  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Artificial  
 W--> 31 <220> FEATURE:  
 W--> 33 <221> NAME/KEY: antisense  
 34 <222> LOCATION: (1)..(20)  
 35 <223> OTHER INFORMATION: antisense  
 38 <400> SEQUENCE: 1  
 39 tgacgcctcc ggagctgaga  
 42 <210> SEQ ID NO: 2  
 43 <211> LENGTH: 20  
 44 <212> TYPE: DNA  
 45 <213> ORGANISM: Artificial  
 W--> 46 <220> FEATURE:  
 W--> 49 <221> NAME/KEY: antisense  
 50 <222> LOCATION: (1)..(20)  
 51 <223> OTHER INFORMATION: antisense  
 54 <400> SEQUENCE: 2  
 55 tgacgcctct ggagctgagc  
 59 <210> SEQ ID NO: 3  
 60 <211> LENGTH: 30  
 61 <212> TYPE: DNA  
 62 <213> ORGANISM: Artificial  
 64 <220> FEATURE:  
 65 <221> NAME/KEY: primer\_bind  
 66 <222> LOCATION: (1)..(30)  
 67 <223> OTHER INFORMATION: primer\_bind  
 70 <400> SEQUENCE: 3  
 71 cgcgatcca tggctgagta cgggaccctc

pp 1-2

Does Not Comply  
corrected Diskette Needs

insufficient explanation - give source of  
 genetic material  
 (see item 11 on  
 Error summary  
 sheet)

same error

this doesn't explain source

## RAW SEQUENCE LISTING

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DATE: 12/16/2005

TIME: 15:34:28

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12162005\J559627.raw

74 <210> SEQ ID NO: 4  
75 <211> LENGTH: 43  
76 <212> TYPE: DNA  
77 <213> ORGANISM: Artificial  
79 <220> FEATURE:  
80 <221> NAME/KEY: primer\_bind  
81 <222> LOCATION: (1)..(43)  
82 <223> OTHER INFORMATION: primer\_bind  
84 <400> SEQUENCE: 4  
85 ggcctttcttc ggtgggggag ccaatttgat gatctcttcc tca

43

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/559,627

DATE: 12/16/2005  
TIME: 15:34:29

Input Set : A:\seq list.txt  
Output Set: N:\CRF4\12162005\J559627.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/559,627

DATE: 12/16/2005

TIME: 15:34:29

Input Set : A:\seq list.txt

Output Set: N:\CRF4\12162005\J559627.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:31 M:283 W: Missing Blank Line separator, <220> field identifier  
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1  
L:46 M:283 W: Missing Blank Line separator, <220> field identifier  
L:49 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2